

BEST AVAILABLE COPY

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to:

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

On April 28, 2005

TOWNSEND and TOWNSEND and CREW LLP

By: Patricia Anders

PATENT
Attorney Docket No.: 02307E-114910US
Client Ref. No.: 2001-124-2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Zuker et al.

Application No.: 10/026,188

Filed: December 21, 2001

For: ASSAYS FOR TASTE RECEPTOR
CELL SPECIFIC ION CHANNEL

Customer No.: 20350

Confirmation No. 9521

Examiner: Michael T. Brannock

Technology Center/Art Unit: 1646

Declaration of Charles S. Zuker and Yifeng

Zhang pursuant to 37 C. F. R. §1.131

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

We, Charles S. Zuker and Yifeng Zhang, being duly warned that willful false statements and the like are punishable by fine or imprisonment or both, under 18 U.S.C. §1001, and may jeopardize the validity of the patent application or any patent issuing thereon, state and declare as follows:

1. All statements herein made of our own knowledge are true and statements made on information or belief are believed to be true. Exhibits I-V are attached hereto and incorporated herein by reference.

2. At the time this invention was first conceived, we were employees of Howard Hughes Medical Institute and the University of California, located in San Diego, California. All activities described in this Declaration took place in the United States of America.

3. In accordance with 37 C.F.R. §1.131, we state that we completed the claimed invention in the United States prior to April 17, 2000, the filing date of USSN 60/197,491, to which published U.S. Patent Application US 2002/0037515 claims priority.

4. Attached to this Declaration are:

Exhibit I, pages of a printout of a sequence file containing the polynucleotide sequence of 930 clones obtained from a subtracted cDNA library prepared from rat circumvallate cells, following the experimental procedure described in Example I of the application. The pages of Exhibit I indicate the date of last modification to contiguous sequence ("contig") No. 068-3 157 501 and the polynucleotide sequence of clone 501, one of the three clones that make up this contig;

Exhibit II, pages of laboratory notebook indicating that a Blast search was performed for known polynucleotide sequences matching each one of the 930 clones, including clone 501;

Exhibit III, results of sequence alignment between the mouse Trpm5 (also known as Mtr1 and Ltrpc5) and clone 501, which indicate a high degree of homology;

Exhibit IV, polynucleotide sequences of the mouse Trpm5 (GenBank No. NM_020277, derived from GenBank No. AJ271092, see page 2 of printout for NM_020277) and human Mtr1 (GenBank No. AF177473), which indicate that these sequences were publicly accessible by January 14, 2000 (see page 1 of printout for AJ271092) and August 13, 1999 (see page 1 of printout for AF177473), respectively. Exhibit IV further includes results of a sequence alignment between the amino acid sequences encoded by mouse Trpm5 gene and human Mtr1 gene; and

Exhibit V, results of an *in situ* hybridization experiment indicating the taste cell-specific expression of the gene from which clone 501 is derived, using a nucleic acid probe specific for clone 501, which was also referred to as 501-PCR46. Some dates in the Exhibits have been redacted. All redacted dates in the Exhibits are prior to April 17, 2000.

5. Conception of the present invention as well as its reduction to practice are evidenced by Exhibits I-IV. The first page of Exhibit I shows that contig No. 068-3 157 501 consists of three clones: 3, 157, and 501, the longest of which is clone 501. The second page shows the polynucleotide sequence of clone 501. The third page establishes the time of last modification made to contig No. 068-3 157 501 and therefore establishes the time when the sequence of clone 501 was determined. Upon determination of the polynucleotide sequence of clone 501, a Blast search was conducted to identify known polynucleotide sequence(s) with high level of sequence homology with clone 501. This is evidenced by Exhibit II.

6. The identification of the mouse Trpm5 gene through this sequence homology-based search is evidenced by Exhibit III, which demonstrates that the mouse Trpm5 and clone 501 are highly homologous. Therefore, one of skill in the art would consider the rat gene from which clone 501 is derived to be the ortholog of mouse Trpm5. Although this particular sequence alignment shown in Exhibit III was performed at the present time, the same result would have been (and was indeed) obtained at the time the initial Blast search was performed. This is because, as evidenced by Exhibit IV, the polynucleotide sequence of mouse Trpm5 was publicly accessible well before April 17, 2000. Furthermore, Exhibit IV establishes that human Mtr1 and mouse Trpm5 have a greater than 84% identity in amino acid sequence. Based on this high level of sequence homology, one of skill in the art would recognize human Mtr1 as the ortholog of mouse Trpm5. In addition, Exhibit IV also demonstrates that the polynucleotide sequence of human Mtr1 gene was publicly available well before April 17, 2000. Thus, a Blast search based on the sequence of clone 501 by the present inventors at the time indicated by Exhibit II necessarily led to the identification of both the human and mouse versions of the Mtr1 gene. Subsequently, *in situ* hybridization was performed to confirm the taste cell-specific expression of the rat version of this gene, shown in Exhibit V. It is therefore established that,

Appl. No. 10/026,188
Declaration under 37 C.F.R. §1.131
Reply to Office Action of November 30, 2004

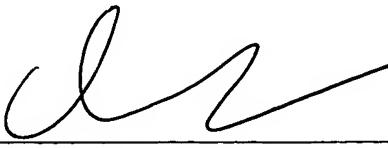
PATENT

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.

7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

Dated: 4/13/05

By: 
Charles S. Zuker, Ph.D.

Dated: _____

By: _____
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)
60427031 V1



Appl. No. 10/026,188

PATENT

Declaration under 37 C.F.R. §1.131

Reply to Office Action of November 30, 2004

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.

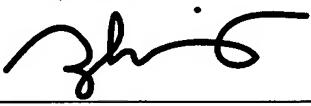
7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

Dated: _____

By: _____
Charles S. Zuker, Ph.D.

Dated: 4/20/05

By: _____
Yifeng Zhang, Ph.D.


Attachments (Exhibits I-V)
60427031 V1

Rat Sub Seq 12/99 copy
Sequencher™ "Rat Sub Seq 12/99 copy"

Name	Size	Kind	Label	Last Modified
042 GS	205 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:58:
043 GS	392 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
044 86	700 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:44:
045	284 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:33:
046 GS	486 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
047	192 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
048 GS	256 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:00:
049 262-5 GS	408 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:07:
050 120 659	571 BPs	Contig of 3	-	Thu, Feb 3, 2000 8:14:
051 854	350 BPs	Contig of 2	-	Thu, Feb 3, 2000 8:14:
052	603 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
053 3'	105 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:32:
053-5 487-5 GS	309 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:49:
053mid 303	268 BPs	Contig of 2	-	Wed, Jan 19, 2000 6:19:
054	502 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:32:
054 5' ok	102 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:09:
055 3' ok	156 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:09:
055 5'	544 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:31:
056	87 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
057 76 178.464 515-...	252 BPs	Contig of 7	-	Thu, Feb 3, 2000 11:1:
059	330 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
060 895-3 ok	307 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:11:
061	43 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
062	453 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
063 GS	222 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:13:
064	609 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
065 3'	85 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:31:
066 5' ok	541 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:16:
067	580 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
068 5' ok	117 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:17:
068 3 157 501	629 BPs	Contig of 3	-	
069 GS	209 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:19:
070 493-5 648-5	351 BPs	Contig of 3	-	Thu, Feb 3, 2000 11:1:
071	560 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
072 3'	104 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:30:
072 5'	578 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:30:
073 815-3	544 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:49:
074 GS	439 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:20:
075 510 229 831 88...	322 BPs	Contig of 6	-	Wed, Jan 19, 2000 6:19:
078 GS	587 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:22:

Differential Screening + Sequencing

Colony lifts w/ blue-white selection

Hybrid N+ lifts
autoclave 5'
rinse to get rid of the debris

Hyb: w/ sub- (reverse subtracted) as probe.

Pick white colonies (930)
Unlighted-up

Miniprep (Clontech 96)

Sequencing (5 μl of each DNA sample)

Report

930 Seg rxn

74 bad seg

856 good or seg

57 have
≥ 2 pieces of inserts

799 have only one inserts

total 933 DNA fragments (w/ seg)

104 contigs

80 pairs

16 triplets

2 contig of 4

1 contig of 5

2 contig of 6

1 contig of 7

2 contig of 9

655 unique DNA fragments

325 unknown by some hits

61 no hits

12 w/ >1 spec. hit (none of them g

8 have full length homologs w/ unknown functions, but no TM at all

9 full length homologs, unknown function
≥ 1 TM

others known genes

(Continued)

II. SF-G15 ~~Euro Assay~~

Not Working !!

Cell lines tried

① Peak Rapid Rb Gx15

② Peak Rapid



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

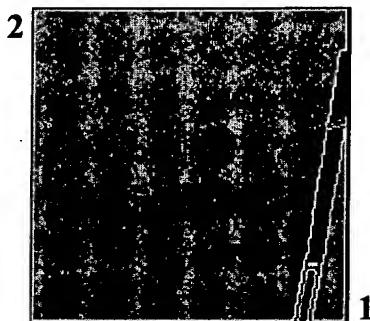
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter

Sequence 1	gi 12383053	Mus musculus transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA	Length 4032 (1.. 4032)
Sequence 2	lcl 501	contig	Length 627 (1.. 627)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 371 bits (193), Expect = 7e-99
 Identities = 349/414 (84%), Gaps = 9/414 (2%)
 Strand = Plus / Plus

Query: 3583 ccttgctacagatcaacttcttggacatcccttcctaagagaatgaaaactcatgtcttgg 3642
 Sbjct: 127 ccttgccgcagaccatgtcttggacacctcttcatatgaaaatgagactcatgtcttgg 186

Query: 3643 catctattcgggagcctcagaagtatcctctccagcaggcaagatttcatgtccac 3702
 Sbjct: 187 catctatctggagccccaggcgt--cctctccagcaggggaagtttctcatgtcctac 244

Query: 3703 -taaagctttcaactggcttggactggacagctggatctggccaagtccatacataggacac 3761
 Sbjct: 248 -taaagctttcaactggcttggactggacagctggatctggccaagtccatacataggacac 3761

Sbjct: 245 ctaaaaactttcaccagctaagactggacagctggaactggccaagtcccacatgggatac 304

Query: 3762 catctgcctggatgggctatttaggtctaaccctgtcttaccctgagttcctaagaag 3821

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 305 catctgcctggatgggctacttacgtctagcc--tgtcttaccctgagttccaaagagg 362

Query: 3822 ccaacaccttaaacactag--gtttcttc-gaccctgaccactcattagctgacca 3878

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 363 ccaacaccttaaacactagactagaggttccttctgtcctctgatccatccatcagccgacca 422

Query: 3879 gctcctagagggcaggactcagatctattgttaattacccatcttcacccccacag 3938

||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 423 gcttctagagggcaggactcagatctactgttaatcagctccatcctcagccccacag 482

Query: 3939 cattatctgtctgatcattctggca-gaaacccaagatattgctcaagggtac 3991

||| ||| ||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 483 cataatttgtgtatygtcctggcacaaaacccaagatactgytcaagggtac 536

Score = 160 bits (83), Expect = 3e-35

Identities = 114/127 (89%), Gaps = 1/127 (0%)

Strand = Plus / Plus



Query: 3442 acctagagtctggcttgcacccctctgacacctgaaatggagaaaccacttgctctagag 3501

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 1 acctagaggctggcttgcacactcagacacctgaaatggagaaaccacttgccctagag 60

Query: 3502 ccccagacacctggccacatcgagtttgggcacatcaaccccccactccagc 3561

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 61 ctccagacacctggccagattgagtttggtcacatcaacccctgc-cccagc 119

Query: 3562 cccaaaga 3568

||| |||

Sbjct: 120 cccgaga 126

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped

Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1
Number of Hits to DB: 69
Number of extensions: 11
Number of successful extensions: 8
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 4032
Length of database: 13,373,181,452
Length adjustment: 27
Effective length of query: 4005
Effective length of database: 13,373,181,425
Effective search space: 53559591607125
Effective search space used: 53559591607125
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 22 (43.0 bits)


[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [OMIM](#) [Books](#)
Search **Nucleotide** **for** **Go** **Clear**
[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)
Display [GenBank](#) [Send](#) [all to file](#)

Range: from to Reverse complemented strand Features: SNP CDD
 MGC HPRD

1: [NM_020277](#). Reports *Mus musculus* tran...[gi:12383053]

[Links](#)

LOCUS NM_020277 4032 bp mRNA linear ROD 26-OCT-2004
DEFINITION *Mus musculus* transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA.
ACCESSION NM_020277
VERSION NM_020277.1 GI:12383053
KEYWORDS
SOURCE *Mus musculus* (house mouse)
ORGANISM *Mus musculus*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4032)
AUTHORS Liu,D. and Liman,E.R.
TITLE Intracellular Ca²⁺ and the phospholipid PIP2 regulate the taste transduction ion channel TRPM5
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (25), 15160-15165 (2003)
PUBMED [14657398](#)
REMARK GeneRIF: regulation of TRPM5 by Ca²⁺ mediates sensory activation in the taste system
REFERENCE 2 (bases 1 to 4032)
AUTHORS Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.
TITLE TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel
JOURNAL Curr. Biol. 13 (13), 1153-1158 (2003)
PUBMED [12842017](#)
REFERENCE 3 (bases 1 to 4032)
AUTHORS Perez,C.A., Huang,L., Rong,M., Kozak,J.A., Preuss,A.K., Zhang,H., Max,M. and Margolskee,R.F.
TITLE A transient receptor potential channel expressed in taste receptor cells
JOURNAL Nat. Neurosci. 5 (11), 1169-1176 (2002)
PUBMED [12368808](#)
REMARK GeneRIF: functions as a cationic channel that is gated when internal calcium stores are depleted and may be responsible for capacitative calcium entry in taste receptor cells that respond to bitter and/or sweet compounds.
REFERENCE 4 (bases 1 to 4032)
AUTHORS Paulsen,M., El-Maarri,O., Engemann,S., Strodicke,M., Franck,O., Davies,K., Reinhardt,R., Reik,W. and Walter,J.
TITLE Sequence conservation and variability of imprinting in the Beckwith-Wiedemann syndrome gene cluster in human and mouse
JOURNAL Hum. Mol. Genet. 9 (12), 1829-1841 (2000)
PUBMED [10915772](#)
REFERENCE 5 (bases 1 to 4032)
AUTHORS Enklaar,T., Esswein,M., Oswald,M., Hilbert,K., Winterpacht,A., Higgins,M., Zabel,B. and Prawitt,D.
TITLE Mtr1, a novel biallelically expressed gene in the center of the mouse distal chromosome 7 imprinting cluster, is a member of the Trp gene family

JOURNAL Genomics 67 (2), 179-187 (2000)
 PUBMED 10903843
 REFERENCE 6 (bases 1 to 4032)
 AUTHORS Yatsuki,H., Watanabe,H., Hattori,M., Joh,K., Soejima,H., Komoda,H.,
 Xin,Z., Zhu,X., Higashimoto,K., Nishimura,M., Kuratomi,S.,
 Sasaki,H., Sakaki,Y. and Mukai,T.
 TITLE Sequence-based structural features between Kvlqt1 and Tapal on
 mouse chromosome 7F4/F5 corresponding to the Beckwith-Wiedemann
 syndrome region on human 11p15.5: long-stretches of unusually well
 conserved intronic sequences of kvlqt1 between mouse and human
 DNA Res. 7 (3), 195-206 (2000)
 PUBMED 10907850
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from AJ271092.2.
 FEATURES Location/Qualifiers
 source 1..4032
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129/Sv"
 /db_xref="taxon:10090"
 /chromosome="7"
 gene 1..4032
 /gene="Trpm5"
 /note="synonyms: Mtr1, Ltrpc5, 9430099A16Rik"
 /db_xref="GeneID:56843"
 /db_xref="MGI:1861718"
 CDS 1..3447
 /gene="Trpm5"
 /function="TRP channel"
 /note="long transient receptor potential-related channel
 5;
 go_component: integral to membrane [goid 0016021]
 [evidence ISS] [pmid 10915772];
 go_function: receptor activity [goid 0004872] [evidence
 IEA];
 go_function: ion channel activity [goid 0005216] [evidence
 IEA];
 go_process: transport [goid 0006810] [evidence IEA];
 go_process: ion transport [goid 0006811] [evidence IEA]"
 /codon_start=1
 /product="transient receptor potential cation channel,
 subfamily M, member 5"
 /protein_id="NP_064673.1"
 /db_xref="GI:12383054"
 /db_xref="GeneID:56843"
 /db_xref="MGI:1861718"
 /translation="MQTTQSSCPGSPPDTEDGWEPILCRGEINFGGSGKKRGKFVKVP
 SSVAPSVLFELLTEWHPAPNLVSVLVGEERPLAMKSWLDRVLRKGLVAAQSTGAW
 ILTSALHVGLARHVGQAVRDHSILASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDT
 PIHYPADEGNIQGPLCPLDSNLSHFILEVESGALGSGNDGLTELQLSLEKHISQQRTGY
 GGTSCIQIPVLCLLVNGDPNTLERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLL
 VPQVAEKQFREKFPSECFSWEAIVHWTELLQNIAAHPHLLTVYDFEQEGSEDLDTVIL
 KALVKACKSHSQEAQDYDELKLAVAWDRVDAIKSEIFNGDVWKSCDLEEVMTDALV
 SNKPDFVRLFDGADMAEFLTYGRLQQLYHSVSPKSLLFELLQRKHEEGRRTLQAGLG
 AQQARELPGLPAFSLHEVSRVLKDFLHDACRGFYQDGRRMEERGPPKRPGQKWLPD
 LSRKSEDPWRDLFLWAVLQNRYEMATYFWAMREGVAAALAACKIIKEMSHLEKEAEV
 ARTMREAKYEQLALDLFSECYGNSEDRAFALLVRRNHWSRTCLPLATEADAKAFFA
 HDGVQAFLTKIWWGDMATGTPILRLLGAFTCPALIYTNLISFSEDAPQRMDLEDLQEP
 DSLDMEKSFLCSRGGQLEKLTEAPRAPGDLGPQAAFLLTRWRKFWGAPVTFLGNVVM
 YFAFLFLFTYVLLVDFRPPPQGPGSEVTLYFWVFTLVLEEIRQGFFTDEDTHLVKKF
 TLYVEDNWNKCDMVAIFLFIVGVTCRMPSVFEAGRIVLAIDFMVFTLRLIHFIAHK
 QLGPKIIIIVERMMKDVFVFFLFLSVWLVAYGVTTQALLHPHDGRLEWIFRRVLYRPYL
 QIFGQIPLDEIDEARVNCSLHPLLLESSASCPNLYANWLVILLVTFLVTNVLLMNL"

LIAMFSYTFQVVQGNADMPWKFQRYHLIVEYHGRPALAPPFILLSHLSVLKQVFRKE
 AQHKRQHLERDLPDPLDQKIIWTWETVQKENFLSTMEKRRRDSEGEVLRKTAHRVDLIA
 KYIGGLREQEKRICKLESQANYCMLLLSSMTDTLAPGGTYSALRTVVAGVSQPLLETG
 ST"

ORIGIN

```

1 atgcaaacaa cccagagctc ctgccccggc agccccccag atactgagga tggctggag
 61 cccatcttat gcaggggaga gatcaacttc ggagggtctg ggaagaagcg aggcaagttt
 121 gtgaaggtgc caagcagtgt ggccccctcc gtgttttg aactcctgct caccgagtgg
 181 cacctgccag ccccaacact ggtgggtgtcc ctgggtgggtg aggaacgacc ttggctatg
 241 aagtctgtgc ttccggatgt cctgcgcaag gggctggta aagcagctca gagcacaggt
 301 gcctgatcc tgaccagtgc ctcacgtg ggcctggccc gccatgttgg acaagctgt
 361 cgtgatcaact ctctggcttag cacatccacc aagatccgtg tagtggccat cgaaatggcc
 421 tctctggatc gaatccttca ccgtcaactt cttagatgtg tccacccaaa ggaggatact
 481 cccatccact acccagcaga tgagggcaac attcaggac ccctctgccc cctggacagc
 541 aatctctccc acttcatcct tgtggagtca ggccccttgg gtagtggaa cgacgggctg
 601 acagagctgc agctgagcct ggagaagcac atctctcagc agaggacagg ttatggggc
 661 accagctgca tccagatacc tgcctttgc ctgtgggtca atggtgaccc caacacccta
 721 gagaggatt ccagggcagt ggagcaggct gccccatggc tgatcctggc aggttctggt
 781 ggcattgtcg atgtactcgc tgccctgggt agccagcctc atctcctggt gccccaggtg
 841 gctgagaagc agttcagaga gaaattcccc agcgagtgtt tctttggga agccattgt
 901 cactggacag agctgttaca gaacattgtc gcacaccccc acctgctcac agtataatgac
 961 ttcgagcagg agggttcgga ggacctggac actgtcatcc tcaaggact tgtgaaagcc
1021 tgcaagagcc acagccaaga agcccaagac tacctagatg agctcaagtt agcagtggcc
1081 tgggatcgcg tggacattgc caagagtga atcttcaatg gggacgtggaa atggaaagtcc
1141 tggacttgg aagaggtgtat gacagatgcc ctcgtgagca acaagcctga ctttgcgc
1201 ctcttgggg acagcgggtgc tgacatggcc gagttcttgc cctatggcg gctgcagcag
1261 ctaccatt ctgtgtcccc caagagcctc ctcttgcac tgctgcagcg taagcatgag
1321 gagggtaggc tgacactggc cggcctgggt gcccagcagg ctcggggagct gcccattgg
1381 ctgcctgcct ttcacttcca cgaggctctcc cgcgtactca aagacttccct gcatgacgcc
1441 tgcctggct ttcaccaggaa cggcgcgcagg atggaggaga gagggccacc taagcggccc
1501 gcaggccaga agtggctgcc agaccccttgtt aggaagagtg aagacccttgg gaggacactg
1561 ttcctctggg ctgtgtgcga gaatcggtat gagatggcca cataacttctg gcccatggc
1621 cgggagggtg tggctgtgc tctggctgcc tgcaagatca taaaggaaat gtcccacactg
1681 gagaagagg cagagggtggc cgcaccatg cgtgaggccca agttagagca gctggccctg
1741 gatctttctc cagagtgcata cggcaacagt gaggaccgtg ccttgccttgc gctggcgc
1801 aggaaccaca gctggagcag gaccacgtgc ctgccttgg ccactgaaagc tgatgccaag
1861 gcctcttttgc cccatgcagg tggcaagca ttcctgacca agatctggg gggagacatg
1921 gccacaggca caccatccct acggcttgc ggtgccttca cctgcccagg cctcatctac
1981 acaaaccata ttccttcag tgaggatgcc cgcagagga tggacctaga agatctgcag
2041 gagccagaca gctggatat ggaaaaagac ttcctatgc gcccgggtgg ccaattggag
2101 aagctaacag aggcaccaag ggctccaggc gatctaggcc cacaagctgc ttcctgtctc
2161 acacgggtggaa ggaagttctg gggcgcttgc tgactgtgt tcctggggaa tgggtcata
2221 tacttcgcata ttccttcctt gttcacctat gtcctgtgg tggacttcag gccaccaccc
2281 cagggccgt ctggatccga gtttaccctc tatttctggg tggacttgc ggtgctggag
2341 gaaatccgac agggcttctt cacagatgag gacacgcacc tggtaagaa attactctg
2401 tatgtggaa gcaactggaa caagtgtgac atgggtggca tcttcctgtt cattgtggaa
2461 gtcacctgtat gatatgggtcc ctcgggtttt gaggctggca ggaccgttctt ggcatttgac
2521 ttcatgggtgt tcacacttgc gtcatccac atcttgcata ttcacaagca gttgggtcct
2581 aagatcatca ttgttagagcg aatgtatgaa gatgtcttctt ttttccttgc cttcctgagc
2641 gatggcttgc tggcctatgg tggaccact caggccctgc tgcatccccca tggatggccgt
2701 ttggagtgaa tttccggcc tggctatac aggccttacc tgcatgtttt tggccaaatc
2761 cctctggatg aaattgtatgaa ggctcggtg aactgttctc ttcacccttgc gctgctggaa
2821 agctggctt cctggccctaa tctctatgccc aactggctgg tcatcttgc gctgggttacc
2881 ttccctgttgc tcaaatgtt gctgctcatg aaccttctgaa tcggcatgtt cagctacaca
2941 ttccagggtgg tgcaaggcaaa tgcaagatgt ttctggaaat ttcaacgtca ccacccatc
3001 gttgaataacc atggaagacc agctctggcc cggcccttca tcctgtctc ccacccatc
3061 ctgggtgtca agcagggtctt caggaaggaa gcccagcata agcgacaaca tctggagaga
3121 gacttgcctg accccttggaa ccagaagatc attacctggg aaacgggttca aaaggagaac
3181 ttcctgagta ccatggagaa acggaggagg gacagcggagg gggaggtgtc gaggaaaacg
3241 gcacacagag tggacttgcata tgccaaatac atcggtggcc tgagagagca agaaaagagg
3301 atcaagtgtc tggaaatcaca ggccaactac tggatgtcc tcttgcctc tatgacggat
3361 acactggctc caggaggcac ctactcagct ctcagaactg tgggtgcagg agtcagccag
3421 cctctgttag agacagggag tacctagatg ctggcttgc accctctgac acctgaaatc

```

3481 gagaaccac ttgctctaga gccccagacc tggccacatc gagttttgg ggcacatcaa
3541 cttccccca ctcccagcac ccccaagaaa tggtcttcaa ggccttgcta cagatcaatt
3601 cttggacatc ctttcctaag agaatgaaac tcatagtctt ggcatactt cgggagcctc
3661 agaagtatcc tctccagcag ggcaagattt ttcatgtccc actaaagctt tcactggctt
3721 ggactggaca gctggatctg gccaagtctt acataggaca ccatactgcctt ggatggggct
3781 atttaggtct aaccctgtc ttaccctgag ttccataagaa gccaacctct taaacactag
3841 gtttcttct gaccctgac ccactcatta gctgaccgc tccttagaggg caggactcag
3901 atctattgtt attacctccc atcttcacc ccccacagca ttatctgtct gatcattctg
3961 gcagaaaccc caagatattt ctcaaggta cccaatgcta ctttactttc tataaagcct
4021 gtagaccacc tc

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search **Nucleotide** for

Limits Preview/Index History Clipboard Details

Display GenBank all to file

Range: from to Reverse complemented strand Features: SNP CDD
 MGC HPRD

1: [AJ271092](#). Reports ...[gi:8546859] The record has been replaced by [AJ271092.2](#)

LOCUS MMU271092 4691 bp mRNA linear ROD 03-AUG-2000

DEFINITION Mus musculus partial mRNA for Ltrcp5 protein (Ltrpc5 gene).

ACCESSION AJ271092

VERSION AJ271092.1 GI:8546859

KEYWORDS Ltrpc5 gene; Ltrpc5 protein.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4691)

AUTHORS Paulsen,M., El-Maarri,O., Engemann,S., Stroedicke,M., Franck,O.,
Davies,K., Reinhardt,R., Reik,W. and Walter,J.

TITLE Sequence conservation and variability of imprinting in the
beckwith-wiedemann syndrome gene cluster in human and mouse

JOURNAL Hum. Mol. Genet. 9 (12), 1829-1841 (2000)

MEDLINE [20377495](#)

REFERENCE 2 (bases 1 to 4691)

AUTHORS Stroedicke,M.

TITLE Direct Submission

JOURNAL Submitted (14-JAN-2000) Stroedicke M., T.A.Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY

COMMENT [WARNING] On Jan 21, 2001 this sequence was replaced by a newer
version gi:[12329972](#).

FEATURES Location/Qualifiers

source
1..4691
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 SV"
/sub_species="domesticus"
/db_xref="taxon:[10090](#)"
/chromosome="7"

gene
1..3330
/gene="Ltrpc5"

CDS
<1..3330
/gene="Ltrpc5"
/function="TRP channel"
/codon_start=1
/evidence=experimental
/product="Ltrpc5 protein"
/protein_id="CAB94717.1"
/db_xref="GI:[8546860](#)"
/translation="MQTTQSSCPGSPPDTEDGWEPILCRGEINFGGSGKKRGKFVKVP
SSVAPSVLFELLTEWHLPAPNLVSVLGEERPLAMKSWLRDVLRKGLVKAQSTGAW
ILTSALHVGLARHVQAVRDHSI LASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDT
PIHYPADEGNIQGPLCPLDSNLSHFILVESGALGSGNDGLTELQLSLEKHISQQRTGY
GGTSCIQIPVLCLLVNGDPNTLERISRRAVEQAAPWLILAGSGGIADVLAALVSQPHLL
VPQVAEKQFREKFPECFWSWEAIVHWTELLQNIAAHPHLLTVYDFEQEGSEDLDTVIL

KALVKACKSHSQEAQDYLDELKLAVALDRVDIAKSEIFNGDVEWKSCDLEEVMTDALV
 SNKPDFVRLFVDSGADMAEFLTYGRLQQLYHSVSPKSLLFELLQRKHEEGRLTLAGLG
 AQQARELPILPAFLSHEVSRVLKDFLHDACRGFYQDGRRMEERGPPKRPAQKWLPP
 LSLRKSEDPWDLFLWAVLQNRYEMATYFWAMREGVAALAACKIIKEMSHLEKEAEV
 ARTMREAKYEQLALDLFSECYGNSEDRAFALLVRRNHSWSRTCLHLATEADAKAFFA
 HDGVQAFLTAKIWWGDMATGTPILRLLGAFTCPALIYTNLISFSEDAPQRMDLEDLQEP
 DSLDMEKSFLCSRGGQLEKLTEAPRAPGDLGPQAAFLLTRWRKFVWAPTVFLGNVVM
 YFAFLFLFTYVLLVDFRPPPQGPGSEVTLYFWVFTLVLEEIRQGFTDEDTHLVKKF
 TLYVEDNWNKCDMVAIFLFIVGVTCRMPSVFEAGRTVLAIDFMVFTLRLIHIFAIHK
 QLGPKIIIVERMMKDVFVFLFLSVWLVAYGVTQALLHPHDGRLEWIFRRVLYRPYL
 QIFGQIPLDEIDEARVNCSLHPLLLESSASCPNLYANWLVILLVTNVLLMNLL
 LIAMFSYTFQVVQGNADMFWKFRYHLLIVEYHGRPALAPPFILLSHLSLVLKQVFRKE
 AQHKRQHLERDLPDLDQKIIWTWETVQKENFLSTMEKRRDSEGEVLRKTAHRVDLIA
 KYIGGLREQEKRIKCLEQSAS"

ORIGIN

```

1 atgcaaacaa cccagagctc ctgccccggc agccccccag atactgagga tggctggag
61 cccatcctat gcagggggaga gatcaacttc ggagggtctg ggaagaagcg aggcaagttt
121 gtgaaggtgc caagcagtgt ggccccctcc gtgcttttg aactcctgtc caccgagtgg
181 cacctgccag cccccaacctt ggtggtgtcc ctgggtgggtt aggaacgacc ttggctatg
241 aagtctggc ttccggatgt cctgcgcaag gggctggta aagcagctca gagcacaggt
301 gcctggatcc tgaccagtgc cctccacgtg ggcctggccc gccatgttgg acaagctgt
361 cgtgatcact ctctggctag cacatccacc aagatccgtg tagtggccat cggaatggcc
421 tctctggatc gaatccttca cctgtcaactt cttagatgggtt tccacccaaa ggaggatact
481 cccatccact acccagcaga tgagggcaac attcaggac ccctctgccc cctggacagc
541 aatctctccc acttcatcct tggatgtca ggcgccttg ggagtggaa cgacgggctg
601 acagagctgc agctgagcct ggagaagcac atctctcagc agaggacagg ttatggggc
661 accagctgca tccagatacc tggatgtcc ctgggtgtca atggtgcacc caacacccctt
721 gagaggattt ccagggcagt ggagcaggct gccccatggc tggatctggc aggttctgg
781 ggcattgctg atgtactcgc tggccctgggt agccagccctc atctctgggtt gccccaggtg
841 gctgagaagc agttcagaga gaaattcccc agcgagtgtt tggatctgggaa agccattgtt
901 cactggacag agctgttaca gaaacattgtt gcacacccccc acctgctcac agtataatgac
961 ttcgagcagg agggttcgga ggacccggac actgtcatcc tcaaggcact tggatggcc
1021 tgcaagagcc acagccaaga agcccaagac taccttagatg agctcaagttt agcagtggcc
1081 tgggatcgcg tggacattgc caagagtggaa atcttcaatg gggacgtggaa atggaaagtcc
1141 tgtgacttgg aagagggtat gacagatgcc ctcgtgagca acaagcctga ctttgcgc
1201 ctctttgtgg acagcgggtgc tgacatggcc gagttcttgc cctatggggc gctgcagcag
1261 ctaccattt ctgtgtcccc caagagccctc ctcttgcac tggatctggc taagcatgag
1321 gagggtaggc tgacactggc cggccctgggt gcccagcagg ctcggagct gcccattgg
1381 ctgcctgcct tctacttca cggggctcc cgcgtactca aagacttcct gcatgacgccc
1441 tgccgtggct tctaccaggaa cggggcgcagg atggaggaga gagggccacc taagcggccc
1501 gcagggcaga agtggctgcc agacccctgtt aggaagagtg aagacccctt gaggggacactg
1561 ttcctctggg ctgtgtgcgaa atcttgcac tggatctggc cataacttgc ggcacatggg
1621 cgggagggtt tggatctgc tctggctgcc tgcaagatca taaaggaaat gtcacccctt
1681 gagaaagagg cagagggtggc cccgccccatg cgtgaggccca agtatgagca gctggccctt
1741 gatctttctt cagagtgcata cggcaacactt gaggaccgtt ctttgcctt gctggatgc
1801 aggaaccaca gctggagcag gaccacgtc ctgcacccctt ccactgaagc tgatgccaag
1861 gccttcttgc cccatgacgg tggatgtca ttcctgcacca agatctgggtt gggagacatg
1921 gccacaggca caccatccctt acggcccttgc ggtgccttca cctgcccaccc cctcatctac
1981 acaaacctca tctcccttgc tggatgtcc cccgccccatg tggacccatggaa agatctgc
2041 gagccagaca gctggatata gaaaaagagc ttcctatgc tggatctggc gccgggggtgg ccaattggag
2101 aagctaacacg aggccaccaag ggctccaggc gatctaggcc cacaagctgc ttcctgtctc
2161 acacgggtggaa ggaagttctt gggccgttgc tggatctggc tggatctgggtt tggatctggc
2221 tacttcgcattt tcccttttgc tggatgtcc tggatctggc tggatctgggtt ggcacccatgg
2281 cagggccgtt ctggatccgc ggttaccctt tggatctggc tggatctgggtt ggtgctggag
2341 gaaatccgac agggcccttgc tggatgtcc cccgccccatg tggatctgggtt ggtgctggag
2401 tatgtggaaat gaaactggaa caagtgtgc tggatctggc tggatctgggtt cattgtggaa
2461 gtcacccgtt gatgtggcc ctcgggtttt gaggctggca ggaccgttcc ggcacccatgg
2521 ttcatgggtt tccatgggtt tccatgggtt tccatgggtt tccatgggtt tccatgggtt
2581 aagatcatca ttgttagagcg aatgtatgc gatgtcttctt ttttccctttt cttccctgagc
2641 gtatggctt tggatctggc tggatctggc tggatctgggtt ggtgctggag
2701 ttggatgtggaa ttttccggcc tggatctggc tggatctggc tggatctgggtt ggtgctggag
2761 cctctggatg aaattgtatgc ggtcgatgtt aactgttctt ttcaccctt ggtgctggaa
2821 agctccgtt ctcggccatcc ttcaccctt ggtgctggc tggatctgggtt ggtgctggag

```

2881 ttccctgcttg tcactaatgt gctgctcatg aaccttctga tcgccatgtt cagctacaca
2941 ttccagggtgg tgcaaggcaa tgcagacatg ttcttggaaat ttcaacgcta ccacccatc
3001 gttgaatacc atggaagacc agctctggcc ccgccttca tcctgcttag ccacctgagc
3061 ctgggtctca agcaggtctt caggaaggaa gcccagcata agcgacaaca tctggagaga
3121 gacttgcctg accccttggaa ccagaagatc attacctggg aaacggttca aaaggagaac
3181 ttccctgatgta ccatggagaa acggaggagg gacagcgagg gggaggtgt gaggaaaacg
3241 gcacacagag tggactttagt tgccaaatac atcgaaaaaa tgagagagca agaaaagagg
3301 atcaagtgtc tggaaatcaca ggcaagctag caactcaacta tccatcttc ttccctgggt
3361 gggggcatcc ttctgggttcc atgggaacta ccacagccct gtaccagcat cctgggggt
3421 agcattaggg cctggataga gtggcctgccc cctgccccaa ctcactttcg agactcattg
3481 ttgttctaga gctggtccaa caaaaacctag gttcagcacc acatccggc actatccctt
3541 atcatgcact atgggaggac ctggccaga gtgtggagtc ccagggcagc agtagccctg
3601 gcaggagggc aatcacatgg gaggaaacca acccggtccc cccagttttt accgaagtct
3661 cagtaacctcc ttggctctc tccaggccaa ctactgtatg ctccttctgt cctctatgac
3721 ggatacactg gctccaggag gcacctactc aagtaagtat gggttcagggc catggaaatg
3781 agatgggtat gggctccccc ttccagccac tagatttaggg caagagcaaa gctgcgggct
3841 gtgtattgtt ttaggtctgt ctttctccac ctgtgtctaga ggtcggttac cttcggcagg
3901 ccactgttcc tttagtgc aaggctctgc ctgcactgg ctttgcctgc cttgcactt
3961 tccatgtctt ggccttggc tcactcttc cctgccccag ctgaggctct ccagctgagg
4021 gtcctttctc ctttcttgc tccaggctc tcagaactgt gggttcagga gtcagccagc
4081 ctctgtttaga gacagggtt accttagatc tggcttgcac ccctctgaca cctgaaatgg
4141 agaaaccact tgctcttagag ccccgacactt ggccacatcg agtttttggg gcacatcaac
4201 cttccccccac tcccagcagc cccaaagaaat ggtcttcaag gccttgcctac agatcactt
4261 ttggacatcc ttccctaaga gaatgaaact catgtctttg gcatcttattc gggagcctca
4321 gaagtatctt ctccagcagg gcaagatttt tcatgtccca ctaaagcttt cactggcttgc
4381 gactggacag ctggatctgg ccaagtccctt cataggacac catctgcctg gatggggctt
4441 ttttaggtctt accccctgtt taccctgttgc tcctttagt tcctttagt ccaacactttt aaacacttagg
4501 tttctttctg accccctgttgc cactcattttt ctgaccatgtt ccttaggggc aggactcaga
4561 tctattgttaa ttacctccca tctttcaccc cccacagcat tatctgtctg atcattctgg
4621 cagaaaccccc aagatattgc tcaagggtac ccaatgttac tttacttttctt ataaaggctt
4681 tagaccaccc c

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10


[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [OMIM](#) [Books](#)
Search **for**
[Limits](#)[Preview/Index](#)[History](#)[Clipboard](#)[Details](#)

Range: from to Reverse complemented strand Features: SNP CDD
 MGC HPRD

1: [AF177473](#). Reports *Homo sapiens* MTR1...[gi:6715116] Links

LOCUS AF177473 3913 bp mRNA linear PRI 20-JAN-2000
DEFINITION *Homo sapiens* MTR1 (MTR1) mRNA, complete cds, alternatively spliced.
ACCESSION AF177473
VERSION AF177473.1 GI:6715116
KEYWORDS
SOURCE *Homo sapiens* (human)
ORGANISM *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3913)
AUTHORS Prawitt,D., Enklaar,T., Klemm,G., Gartner,B., Spangenberg,C., Winterpacht,A., Higgins,M., Pelletier,J. and Zabel,B.
TITLE Identification and characterization of MTR1, a novel gene with homology to melastatin (MLSN1) and the trp gene family located in the BWS-WT2 critical region on chromosome 11p15.5 and showing allele-specific expression
JOURNAL Hum. Mol. Genet. 9 (2), 203-216 (2000)
PUBMED [10607831](#)
REFERENCE 2 (bases 1 to 3913)
AUTHORS Prawitt,D., Pelletier,J. and Zabel,B.U.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1999) Children's Hospital, University of Mainz, Langenbeckstr. 1, Mainz, D 55101, Germany
FEATURES Location/Qualifiers
source
 1..3913
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11p15.5"
gene
 1..3913
 /gene="MTR1"
CDS
 10..3507
 /gene="MTR1"
 /note="MLSN1 and TRP-related putative protein; alternatively spliced"
 /codon_start=1
 /product="MTR1"
 /protein_id="[AAF26288.1](#)"
 /db_xref="GI:6715117"
 /translation="MQDVQGPRPGSPGDAEDRRELGLHRGEVNFGGSGKKRGKFVRVP SGVAPSVLFDLLLAEWHLPAPNLVSLVGEQPFAMKSWLRDVLRKGLVKAQSTGAW ILTSALRVGLARHVQAVRDHSI LASTSTKVRVVAVGMASLGRVLHRRILEEAQEDFPV HYPEDDGGSQGPLCSLDSNLSHFILVEPGPPKGDGGLTELRLRLEKHISEQRAGYGGT GSIEIPVLCLLVNGDPNTLERISRAVEQAAPWLILVGSGGIADVLAALVNQPHLLVPK VAEKQFKEKFPSKHFSEDIVRWTKLQNITSQHLLTVYDFEQEGSEELDTVILKAL VKACKSHSQEPQDYLDDELKLAVALWDRVDIAKSEIFNGDVEWKSCDLEEVMDALVSNK"

PEFVRLFDNGADVADFLTYGRLQELYRSVRKSLLFDLQLRKQEEARLTLAGLGTQO
 AREPPAGPAFSLHEVSRLKDFLQDACPGRGYQDGPGDRRAEKGPARKPTGQKWLL
 DLNQKSENTPWRDLFLWAVLQRHEMATYFWAMGQEGVAAALAACKILKEMSHLETEAE
 AARATREAKYERLALDLFSECYNSSEARAFALLVRRNRCWSKTTCLHLATEADAKAFF
 AHDGVQAFLTRIWWGMDMAAGTPILRLLGAFLCPALVYTNLITFSEEAPLRTGLEDLQD
 LDSLDTEKSPLYGLQSRVEELVEAPRAQGDGRGPRAVFLTRWRKFWGAPVTVFLGNVV
 MYFAFLFLFTYVLLVDFRPPPQGPGSGPEVTLYFWVFTLVLEEIRQGFFTDEDTHLVKK
 FTLYVGDNWNKCDMVAIFLFIVGVTCRMLPSAFEAGRVLAMDFMVFTLRLIHIAH
 KQLGPKIIVERMMKDVFVFFLFLSVWLVAYGVTTQALLHPHDGRLEWIFRRVLYRPY
 LQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILLVTFLTNVLLMN
 LLIAMFSYTFQVVQGNADMFWKFQRYNLIVEYHERPALAPPFILLSHLSLTLLRVFKK
 EAEHKREHLERDLPDLDQKVVTWETVQKENFLSKMEKRRRDSEGEVLRKTAHRVDFI
 AKYLGGLREQEKRICKLESQINYCSVLVSSVADVLAQGGGPRSSQHCGEGLVAAADH
 RGGLDGCWEQPGAGQPPSDT"

ORIGIN

1	gaggccacca	tgcaggatgt	ccaaggcccc	cgtcccgaa	ccccgggaa	tgctgaagac
61	cggcgggagc	ttggccttgc	cagggcgag	gtcaacttg	gagggtctgg	gaagaagcga
121	ggcaagtttg	tacgggtgcc	gacggagtg	ccccgtctg	tgctcttga	cctgctctt
181	gctgagtggc	acctgccgc	ccccaaacctg	gtggtgtccc	tgggggtga	ggagcagcct
241	ttcgccatga	agtcctggct	gcgggatgtg	ctgcgcagg	ggctgggtgaa	ggcggctcag
301	agcacaggag	cctggatcct	gaccagtgcc	ctccgcgtgg	gcctggccag	gcatgtcggg
361	caggccgtgc	gcgaccactc	gctggccagc	acgtccacca	aggccgtgt	ggttgcgtc
421	ggcatggcct	cgctgggccc	cgtcctgcac	cgccgcattc	tggaggaggc	ccaggaggat
481	tttcctgtcc	actaccctga	ggatgacggc	ggcagccagg	ccccctctg	ttcactggac
541	agcaacctct	cccacttcat	cctgggtggag	ccaggcccc	cgggaaaggg	cgatggctg
601	acggagctgc	ggctgaggt	ggagaagcac	atctcgagc	agagggcggg	ctacggggc
661	actggcagca	tgcagatccc	tgtccctctgc	ttgctggta	atggtatacc	caacaccttgc
721	gagaggatct	ccagggccgt	ggagcaggct	ccccgtggc	tgcacttgcgt	aggctcgaaa
781	ggcatcgcgc	atgtgcttgc	tgcccttagt	aaccagcccc	accccttgcgt	ccccaaagggt
841	gccgagaagc	agtttaagga	gaagtcccc	agcaaggatt	tctttggga	ggacatcgtg
901	cgctggacca	agctgctgca	gaacatcacc	tcacaccagc	acctgctcac	cgttatgac
961	ttcgagcagg	agggcctcga	ggagctggac	acggtcattc	tgaaggcgt	gttggaaagcc
1021	tgcaagagcc	acagccagga	gcctcaggac	tatctggat	agctcaagct	ggccgtggcc
1081	ttggaccgcg	tggacatcgc	caagagttag	atcttcaatg	gggacgtgg	gttggaaagtcc
1141	tgtgacctgg	aggaggtgat	ggtgacgccc	ctggtcagca	acaagcccc	gtttgtgcgc
1201	ctctttgtgg	acaacggcgc	agacgtggcc	gacttctgta	cgtatggcgc	gtgcaggag
1261	ctctaccgc	ccgtgtcacg	caagagcctg	ctcttcgacc	tgctgcagcg	gaagcaggag
1321	gaggccccgc	tgacgctggc	cgccctgggc	acccagcagg	ccccggagcc	acccgggggg
1381	ccacccgcct	tctccctgca	cgaggctctc	cgcgtactca	aggacttcct	gcaggacgccc
1441	tgccgaggct	tctaccagg	cgccggccca	ggggaccgca	ggagggcgg	gaagggcccc
1501	gccaagccgc	ccacgggcca	gaagtggctg	ctggacctga	accagaagag	cgagaaccccc
1561	tggcgggacc	tgttccctgt	ggccgtgtc	cagaaccgccc	acgagatggc	cacctacttc
1621	tgggccatgg	gccaggaagg	tgtggcagcc	gcactggccg	cctgc当地	cctcaaagag
1681	atgtcgacc	tggagacgga	ggccgaggcg	gcccgagcca	cgcgcaggc	gaaatacag
1741	cggctggccc	ttgaccttct	ctccgagtc	tacagcaaca	gtgaggcccg	cgccttcgc
1801	ctgctgggtc	gccggaaccg	ctgctggagc	aagaccaccc	gcctgcaccc	ggccaccgg
1861	gctgacgcca	aggccttctt	tgcctccagc	ggcgttcagg	ccttcctgac	caggatctgg
1921	tggggggaca	tggccgcagg	cacgccccatc	ctgcggctgc	taggagcctt	cctctggccc
1981	gccctcgct	ataccaacct	catcaccc	agtggagaa	ctccctgt	gacaggcctg
2041	gaggacctgc	aggacctgga	cagccctggac	acggagaaga	ccccgtgt	tggcctgcag
2101	agccgggtgg	aggagctgg	ggaggcggcc	agggctcagg	gtgaccgagg	cccacgtgct
2161	gtcttcctgc	tcacacgctg	gcggaaaattc	tggggcgtc	ccgtactgt	gttcctgggg
2221	aacgtggtca	tgtacttcgc	cttcccttcc	ctgttaccc	acgtcctgt	gttggacttc
2281	aggccccc	cccaggcccc	ctcaggcccc	gaggtcaccc	tctacttctg	ggtctttacg
2341	ctggtgctgg	aggaaatccg	gcagggcttc	ttcacagacg	aggacacaca	cctggtgaag
2401	aagttcacac	tgtatgtgg	ggacaactgg	aacaagtgt	acatggggc	cacccaccca
2461	ttcatacggt	gtgtcacctg	caggatgtg	ccgtccggcgt	ttgaggctgg	ccgcacggc
2521	ctcgccatgg	acttcatgg	gttcaacgt	ccgctgtatcc	atatcttgc	catacacaag
2581	cagctggccc	ccaagatcat	cgtggtagag	cgcacgtatg	aggacgttcc	cttcttc
2641	ttctttctga	gcgtgtggct	cgtggcctac	ggtgtcacca	cccaggcgt	gctgcaccc
2701	catgacggcc	gcctggagtg	gatctccgc	cgggtgtct	accggcccta	cctgcagatc
2761	tccggccaga	tcccactgga	cgagattgat	gaagccgtg	tgaactgctc	cacccaccca
2821	ctgctggcgg	aggactcacc	atcctggccc	agcctctatg	ccaactggct	ggtcatcctc

2881 ctgctggtca ctttcctgtt ggtcaccaat gtgctgtca tgaacctgtc catgcgcatt
2941 ttcagctaca cgttccagggt ggtgcagggc aacgcagaca tgttctggaa gttccagcgc
3001 tacaacctga ttgtggagta ccacgagcgc cccgcctgg cccgcctt catcctgctc
3061 agccacctga gcctgacgtc cgcgggtc ttcaagaagg aggctgagca caagcggag
3121 cacctggaga gagacctgcc agaccccctg gaccagaagg tcgtcacctg ggagacagtc
3181 cagaaggaga acttccttag caagatggag aagcgagga gggacagcga gggggaggtg
3241 ctgcggaaaa ccccccacag agtggacttc attgccaagt acctcgaaaa gctgagagag
3301 caagaaaagc gcatcaagtg tctggagtca cagatcaact actgctcggt gctcgtgtcc
3361 tccgtggctg acgtgctggc ccagggtggc ggccccccggaa gctctcagca ctgtggcgag
3421 ggaagccagc tgggtggctgc tgaccacaga ggtggtttag atggctggaa acaaccggg
3481 gctggccagc ctccctcgga cacatgagct gcttggcctg ccacgtgtgg gccacactct
3541 cttagttgg ccaccctgca cgttgtgcac tgacctttgc cgacccctcag cggAACCCCC
3601 cagggggcac cagcccccca gcagacaatg gccctcctgg tgcctcaccac cagaccctca
3661 cccaaaggaa ccgctccttg tccctcctgg cctccccggaa ggcacacgag tgcgtatgggg
3721 ctgtctcccc tgacaggcac aactccccgg gcagaaaacg tgccccaccg catccctacc
3781 tggaaactga ccagcctgca ctgtggaaaa gctggccctg tggcggtacg ggggagcacc
3841 cccatccaga ctgcgaagct gctctgggtc tgcacccacc cctgcccctga cttgtgttgc
3901 ctgacaagag act

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

Align two sequences

Tue Mar 1 21:52:38 "GMT 2005

```
/usr/tmp/seq1.73316.sca : 1158 aa
>Mouse MTR1, 1158 bases, 31D4F27D checksum.          1158 aa vs.
>Human MTR1, 1165 bases, C1D16397 checksum.        1165 aa
scoring matrix: , gap penalties: -12/-2
84.1% identity;           Global alignment score: 6543
```

```

          10      20      30      40      50      60
/usr/t MQTTQSSCPGSPPDTEGWEPILCRGEINFGGSGKKRGKFVKVPSSVAPSVLFELLLTEW
          :: :::: :::: : : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Human   MQDVQGPRPGSPGDAEDRRELGLHRGEVNFGGSGKKRGKFVRVPSGVAPSVLFDLLAEW
          10      20      30      40      50      60

```

```

          70         80         90        100        110        120
/usr/t HLPAPNLVVSLVGEERPLAMKSWLRDVLRKGLVKAQSTGAWILTSALHVGLARHVGQAV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Human   HLPAPNLVVSLVGEEQPFAKMWSLRDVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV
          70         80         90        100        110        120

```

```

          130      140      150      160      170      180
/usr/t RDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDETPIHYPADEGNIQGPLCPLDS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Human   RDHSLASTSTKVRVVAVGMASLGRVLHRRILE--EAQEDFPVHYPEDDGGSQGPLCSLDS
          130      140      150      160      170

```

	190	200	210	220	230	240	
/usr/t	NLSHFILVESGALGGNGDGLTELQLSLEKHISQQRTGYGGTSCIQIPVLCLLVNGDPNTL	::::::: : . : ::::::: : ::::::: .::: . : .::: ::::::: :					
Human	NLSHFILVEPGPPKGK-DGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTL	180	190	200	210	220	230

```

      250      260      270      280      290      300
/usr/t ERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLLVPQVAEKQFREKFPSECFSWEAIV
::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::: :::::: ::::::
Human   ERISRAVEQAAPWLILVGSGGIADVLAALVNQPHLLVPKVAEKQFKEKFPSKHFSWEDIV
      240      250      260      270      280      290

```

```

          310      320      330      340      350      360
/usr/t HWTELLQNIAAHPHLLTVYDFEQEGSELDTVILKALVKACKSHSQEAQDYLDELKLAVALA
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .
Human  RWTKLLQNITSHQHLLTVYDFEQEGSEELDTVILKALVKACKSHSQEPQDYLDELKLAVALA
300      310      320      330      340      350

```

```

          370      380      390      400      410      420
/usr/t WDRVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNKPDFVRLFVDSGADMAEFLTYGRLQQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Human   WDRVDIAKSEIFNGDVEWKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLQE
          360      370      380      390      400      410

```

	430	440	450	460	470	480
/usr/t	LYHSVSPKSLLFELLQRKHEEGLTLAGLGAQQARELPIGLPAFSLHEVSRVLKDFLHDA	:::::::::::	:::::::::::	:::::::::::	:::::::::::	:::::::::::
Human	LYRSVSRKSLLFDLLQRKQEEARLTLAGLGTQQAREPPAGPPAFSLHEVSRVLKDFLQDA	430	430	440	450	460

	490	500	510	520	530		
/usr/t	CRGFYQDGR---RMEERGPPKRPAGQKWLPLSRSRKSEDPWRDLFLWAVLQNRYEMATYF		
Human	CRGFYQDGRPGDRRRAEKGPARKPTGQKWLLDLNQKSENPWRDLFLWAVLQNRRHEMATYF	480	490	500	510	520	530
	540	550	560	570	580	590	
/usr/t	WAMGREGVAAALAACKIIKEMSHLEKEAEVARTMREAKYEQLALDLFSECYGNSEDRafa	
Human	WAMGQEGVAAALAACKILKEMSHLETEAAARATREAKYERLALDLFSECYSNSEARafa	540	550	560	570	580	590
	600	610	620	630	640	650	
/usr/t	LLVRRNHSWSRTTCLHLATEADAKAFFAHDGVQAFLTKIWWGDMATGTPILRLLGAFTCP	
Human	LLVRRNRCWSKTTCLHLATEADAKAFFAHDGVQAFLTRIWWGDMAAGTPILRLLGAFCLP	600	610	620	630	640	650
	660	670	680	690	700	710	
/usr/t	ALIYTNLISFSEDAPQRMDLEDLQEPDSLDMEKSFLCSRGGQLEKLTEAPRAPGDLGPQA	
Human	ALVYTNLITFSEEAPLRTGLEDLQDLDSDLTEKSPLYGLQSRVEELVEAPRAQGDGRGPRA	660	670	680	690	700	710
	720	730	740	750	760	770	
/usr/t	AFLLTRWRKFWGAPVTVFLGNVVVMYFAFLFLFTYVLLVDFRPPPQGPSCGEVTLYFWVFT	
Human	VFLLTRWRKFWGAPVTVFLGNVVVMYFAFLFLFTYVLLVDFRPPPQGPSCGEVTLYFWVFT	720	730	740	750	760	770
	780	790	800	810	820	830	
/usr/t	LVLEEIRQGFFTDEDTHLVKKFTLYVEDNWNKCDMVAIFLFIVGVTCRMVPSVFEAGRtv	
Human	LVLEEIRQGFFTDEDTHLVKKFTLYVGDNWNKCDMVAIFLFIVGVTCRMLPSAFEAGRtv	780	790	800	810	820	830
	840	850	860	870	880	890	
/usr/t	LAIDFMVFTLRLIHIIFAIHKQLGPKIIIVERMMKDVFVFFLFFLSVWLVAYGVTTQALLHP	
Human	LAIDFMVFTLRLIHIIFAIHKQLGPKIIIVERMMKDVFVFFLFFLSVWLVAYGVTTQALLHP	840	850	860	870	880	890
	900	910	920	930	940	950	
/usr/t	HDGRLEWIFRRVLYRPYLQIFGQIPLDEIDEARVNCSLHPLLLESSASCPNLYANWLVIL	
Human	HDGRLEWIFRRVLYRPYLQIFGQIPLDEIDEARVNCSLHPLLLEDSPSCPSLYANWLVIL	900	910	920	930	940	950
	960	970	980	990	1000	1010	
/usr/t	LLVTFLVLTNVLLMNLLIAMFSYTFQVVQGNADMFWKFQRYHLIVEYHGRPALAPPFILL	
Human	LLVTFLVLTNVLLMNLLIAMFSYTFQVVQGNADMFWKFQRYNLIVEYHERPALAPPFILL	960	970	980	990	1000	1010
	1020	1030	1040	1050	1060	1070	
/usr/t	SHSLVVLQVFRKEAQHKRQHLERDLPDPLDKIITWETVQKENFLSTMKERRRDSEGEV	
Human	SHSLTLRRVFKKEAEHKREHLERDLPDPLDKVVTWETVQKENFLSKMEKRRRDSEGEV	1020	1030	1040	1050	1060	1070
	1080	1090	1100	1110	1120	1130	
/usr/t	LRKTAHRVDLIAKYIGGLREQEKRIKCLESQANYCMLLSSMTDTLAPGGTYSSSQNCGC	

Sequence Alignment Output

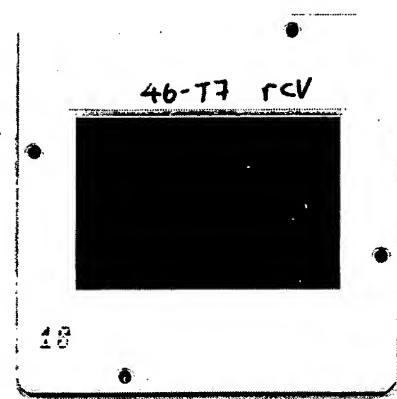
```

Human  LRKTAHRVDFIAKYLGGLREQEKRIKCLSEQINYCSVLVSSVADVLAQGGGPRSSQHCGE
      1080      1090      1100      1110      1120      1130

      1140      1150
/usr/t RSQPASARDREYLE-----SGLPPSDT
      :: . . : . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
Human  GSQQLVAADHRGGLDGWEQPGAGQPPSDT
      1140      1150      1160

```

Elapsed time: 0:00:00





**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.